

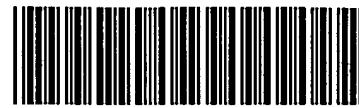
#9

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/528,992
Source: PCT
Date Processed by STIC: 03/31/2006

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RAW SEQUENCE LISTING DATE: 03/31/2006
 PATENT APPLICATION: US/10/528,992 TIME: 11:06:40

Input Set : A:\2006-01-06 0020-5361PUS1.ST25.txt
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3 <110> APPLICANT: Nobuyuki YOSHIDA
 4 Yoshiki TANI
 5 Satoshi YONEHARA
 7 <120> TITLE OF INVENTION: FRUCTOSYLAMINE OXIDASE
 9 <130> FILE REFERENCE: 0020-5361PUS1
 11 <140> CURRENT APPLICATION NUMBER: US 10/528,992
 12 <141> CURRENT FILING DATE: 2005-03-24
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP03/11766
 15 <151> PRIOR FILING DATE: 2003-09-16
 17 <150> PRIOR APPLICATION NUMBER: JP 2002-277214
 18 <151> PRIOR FILING DATE: 2002-09-24
 20 <150> PRIOR APPLICATION NUMBER: JP 2002-309734
 21 <151> PRIOR FILING DATE: 2002-10-24
 23 <160> NUMBER OF SEQ ID NOS: 8
 25 <170> SOFTWARE: PatentIn version 3.1
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 460
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Fusarium proliferatum
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 35 aaaacgggac ggcccgccag aggacccta aactctgtt ctatatgtaa cttctgagta 120
 37 aaaccataaa taaatcaaaa ctttcaacaa cggatcttt ggttctggca tcgatgaaga 180
 39 acgcagcaaa atgcgataag taatgtgaat tgcagaattc agtgaatcat cgaatcttg 240
 41 aacgcacatt ggcggccca gtattctggc gggcatgcct gttcgagcgt catttcaacc 300
 43 ctcaagcccc cgggtttgtt gttggggatc ggcgagccct tgcggcaagc cggccccgaa 360
 45 atcttagtggc ggtctcgctg cagttccat tgcgttagtag taaaaccctc gcaactggta 420
 47 cgcggcgcgg ccaagccgtt aaaccccaa cttctgaatg 460
 50 <210> SEQ ID NO: 2
 51 <211> LENGTH: 10
 52 <212> TYPE: PRT
 53 <213> ORGANISM: Fusarium proliferatum
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 57 1 5 10
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 61 <211> LENGTH: 1422
 62 <212> TYPE: DNA
 63 <213> ORGANISM: Fusarium proliferatum
 65 <220> FEATURE:
 66 <221> NAME/KEY: CDS
 67 <222> LOCATION: (1)..(1419)
 69 <400> SEQUENCE: 3

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71	Met	Ala	Gly	Pro	Pro	Ser	Ser	Ile	Leu	Ile	Val	Gly	Ser	Gly	Val	Phe
72	1			5				10				15				
74	ggg	ctc	ggt	acc	gcc	tgg	gtc	ttt	gcc	aaa	cga	tca	cac	ttt	tcc	96
75	Gly	Leu	Gly	Thr	Ala	Trp	Ala	Leu	Ala	Lys	Arg	Ser	His	Phe	Ser	Asn
76				20				25				30				
78	acc	tcg	att	act	gtc	gtc	gac	tgc	gca	gga	cag	ttt	cct	cca	gaa	144
79	Thr	Ser	Ile	Thr	Val	Val	Asp	Asp	Cys	Ala	Gly	Gln	Phe	Pro	Pro	Glu
80				35			35	40			45					
82	gat	gct	gcc	agt	gtt	gac	tcg	tct	cgc	att	gtt	cga	gac	tac	tcg	192
83	Asp	Ala	Ala	Ser	Val	Asp	Ser	Ser	Arg	Ile	Val	Arg	Ala	Asp	Tyr	Ser
84				50			50	55			60					
86	gac	cct	tac	tat	gcc	gct	ctt	gcc	gag	gct	cag	aag	gaa	tgg	cga	240
87	Asp	Pro	Tyr	Tyr	Ala	Ala	Leu	Ala	Ala	Glu	Ala	Gln	Lys	Glu	Trp	Arg
88				65			70		75			80				
90	aag	cag	ggt	gat	cat	gag	gtc	ggg	cag	gga	cga	tat	tcc	gag	tcg	288
91	Lys	Gln	Gly	Asp	His	Glu	Val	Gly	Gly	Gln	Gly	Arg	Tyr	Ser	Glu	Ser
92				85			85	90			95					
94	ggc	ttt	gtt	ctc	tgc	gct	agc	gag	act	cct	gaa	gac	ttc	aag	ctc	336
95	Gly	Phe	Val	Leu	Cys	Ala	Ser	Glu	Thr	Pro	Glu	Asp	Phe	Lys	Leu	Lys
96				100			100	105			110					
98	aag	tct	ggc	atg	gac	tac	acc	aag	gag	agc	gcc	aaa	aac	gtc	gag	384
99	Lys	Ser	Gly	Met	Asp	Tyr	Thr	Lys	Glu	Ser	Ala	Lys	Asn	Val	Glu	Leu
100				115			115	120			125					
102	att	gct	aag	gag	act	ggt	ctg	ccc	gtg	gat	aag	atc	cag	aag	ctg	432
103	Ile	Ala	Lys	Glu	Thr	Gly	Leu	Pro	Val	Asp	Lys	Ile	Gln	Lys	Leu	Glu
104				130			130	135			140					
106	agt	acc	aag	gct	ctc	caa	gag	ttc	ctt	ggc	aca	gac	ggt	tat	ccc	480
107	Ser	Thr	Lys	Ala	Leu	Gln	Glu	Phe	Leu	Gly	Thr	Asp	Gly	Tyr	Pro	Gly
108				145			145	150			155			160		
110	gac	tgg	ggc	tac	ctc	aat	ggc	aac	tct	ggc	tgg	gct	gat	gcc	ggg	528
111	Asp	Trp	Gly	Tyr	Leu	Asn	Gly	Asn	Ser	Gly	Trp	Ala	Asp	Ala	Gly	Glu
112				165			165	170			175					
114	ggt	atg	aag	tgg	ctc	tat	aag	cag	gcc	cag	gcc	aca	gga	cgt	att	576
115	Gly	Met	Lys	Trp	Leu	Tyr	Lys	Gln	Ala	Gln	Ala	Thr	Gly	Arg	Ile	His
116				180			180	185			190					
118	ttt	gtc	aac	ggc	aag	gtg	aca	gag	ctc	gta	aca	gag	ggt	gac	cga	624
119	Phe	Val	Asn	Gly	Lys	Val	Thr	Glu	Leu	Val	Thr	Glu	Gly	Asp	Arg	Val
120				195			195	200			205					
122	att	ggt	gcg	aaa	ttt	agc	gat	tca	aag	att	ctc	aag	gac	ttt	ggc	672
123	Ile	Gly	Ala	Lys	Leu	Ser	Asp	Ser	Lys	Ile	Leu	Lys	Ala	Asp	Val	Val
124				210			210	215			220					
126	atg	gtt	gct	ggt	gtt	tcc	ggc	tca	ctc	gtt	gac	ttt	cga	gga		720
127	Met	Val	Ala	Ala	Gly	Ala	Trp	Ser	Gly	Ser	Leu	Val	Asp	Leu	Arg	Gly
128				225			225	230			235			240		
130	aga	aca	gag	gct	act	ggc	cat	gct	gtc	gct	tat	atg	gac	atc	aca	768
131	Arg	Thr	Glu	Ala	Thr	Gly	His	Ala	Val	Ala	Tyr	Met	Asp	Ile	Thr	Pro
132				245			245	250			255					
134	gaa	gag	cag	aag	cga	ctc	gac	aac	ttc	cct	gtg	gtg	ttg	aat	ctc	816

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135	Glu	Glu	Gln	Lys	Arg	Leu	Asp	Asn	Phe	Pro	Val	Val	Leu	Asn	Leu	Ser	
136				260					265				270				
138	acc	ggt	ctc	tcc	ctc	att	cct	cct	cga	aat	aac	gtc	ctc	aag	gcc	gcc	864
139	Thr	Gly	Leu	Phe	Leu	Ile	Pro	Pro	Arg	Asn	Asn	Val	Leu	Lys	Ala	Ala	
140				275					280			285					
142	cga	cac	aca	tcc	ggg	tac	att	aac	ccg	gtc	aag	att	aac	aac	gct	ctt	912
143	Arg	His	Thr	Phe	Gly	Tyr	Ile	Asn	Pro	Val	Lys	Ile	Asn	Asn	Ala	Leu	
144				290				295			300						
146	cct	cct	tcg	ccc	aac	gat	aag	cg	gaa	cca	tcc	atc	gca	tct	caa	ccc	960
147	Pro	Pro	Ser	Pro	Asn	Asp	Lys	Arg	Glu	Pro	Phe	Ile	Ala	Ser	Gln	Pro	
148	305				310				315			320					
150	tac	acc	tct	cgc	aac	gat	tcc	tca	aat	cct	tta	acc	gtc	gag	gct	gac	1008
151	Tyr	Thr	Ser	Arg	Asn	Asp	Ser	Ser	Asn	Pro	Leu	Thr	Val	Glu	Ala	Asp	
152					325				330			335					
154	aaa	gat	ctg	cgc	cgc	gca	ctc	acg	gat	ctg	tgt	cct	ata	cgt	ggc	cta	1056
155	Lys	Asp	Leu	Arg	Arg	Ala	Leu	Thr	Asp	Leu	Cys	Pro	Ile	Arg	Gly	Leu	
156					340				345			350					
158	gaa	acc	agg	cca	tgg	aag	gag	gct	cga	atc	tgc	tgg	tat	tcc	gat	aca	1104
159	Glu	Thr	Arg	Pro	Trp	Lys	Glu	Ala	Arg	Ile	Cys	Trp	Tyr	Ser	Asp	Thr	
160					355				360			365					
162	cga	gat	ggc	gag	tgg	ctc	att	gac	tac	cac	ccg	ggc	tgg	aag	gga	ctc	1152
163	Arg	Asp	Gly	Glu	Trp	Leu	Ile	Asp	Tyr	His	Pro	Gly	Trp	Lys	Gly	Leu	
164					370			375			380						
166	ttt	gtt	gca	aca	ggt	gac	agt	gga	cac	gga	tcc	aag	ttc	cta	ccc	aac	1200
167	Phe	Val	Ala	Thr	Gly	Asp	Ser	Gly	His	Gly	Phe	Lys	Phe	Leu	Pro	Asn	
168	385				390				395			400					
170	ttg	gg	aaa	atc	gtg	gat	gtt	atg	caa	ggc	cag	gg	gat	gg	aa	ctt	1248
171	Leu	Gly	Glu	Lys	Ile	Val	Asp	Val	Met	Gln	Gly	Gln	Gly	Lys	Leu		
172					405				410			415					
174	ggc	gag	aag	tgg	cga	tgg	aaa	gag	atc	cag	aat	gat	gga	gtc	gga	aga	1296
175	Gly	Glu	Lys	Trp	Arg	Trp	Lys	Glu	Ile	Gln	Asn	Asp	Gly	Val	Gly	Arg	
176					420				425			430					
178	gag	acg	aac	gga	gtg	tac	act	gg	tta	gtg	acg	gaa	gat	gg	agc	aga	1344
179	Glu	Thr	Asn	Gly	Val	Tyr	Thr	Gly	Leu	Val	Thr	Glu	Asp	Gly	Ser	Arg	
180					435				440			445					
182	gg	gtt	gga	ccg	ccc	ttg	gtg	ctc	tgt	gat	gag	ctc	gag	aag	ggc	agg	1392
183	Gly	Gly	Arg	Pro	Leu	Val	Leu	Cys	Asp	Glu	Leu	Glu	Lys	Gly	Arg	Ala	
184					450			455			460						
186	ctt	att	ggg	aac	acc	aag	gcc	aag	ct	ta	tga						1422
187	Leu	Ile	Gly	Asn	Thr	Lys	Ala	Lys	Leu								
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193	<212>	TYPE:	PRT														
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198	1				5				10			15					
201	Gly	Leu	Gly	Thr	Ala	Trp	Ala	Leu	Ala	Lys	Arg	Ser	His	Phe	Ser	Asn	

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205	Thr Ser Ile Thr Val Val Asp Asp Cys Ala Gly Gln Phe Pro Pro Glu		
206	35	40	45
208	Asp Ala Ala Ser Val Asp Ser Ser Arg Ile Val Arg Ala Asp Tyr Ser		
209	50	55	60
211	Asp Pro Tyr Tyr Ala Ala Leu Ala Ala Glu Ala Gln Lys Glu Trp Arg		
212	65	70	75
214	Lys Gln Gly Asp His Glu Val Gly Gly Gln Gly Arg Tyr Ser Glu Ser		
215	85	90	95
217	Gly Phe Val Leu Cys Ala Ser Glu	Glu	Asp Phe Lys Leu Lys
218	100	105	110
220	Lys Ser Gly Met Asp Tyr Thr Lys Glu Ser Ala Lys Asn Val Glu Leu		
221	115	120	125
223	Ile Ala Lys Glu Thr Gly Leu Pro Val Asp Lys Ile Gln Lys Leu Glu		
224	130	135	140
226	Ser Thr Lys Ala Leu Gln Glu Phe Leu Gly Thr Asp Gly Tyr Pro Gly		
227	145	150	155
229	Asp Trp Gly Tyr Leu Asn Gly Asn Ser Gly Trp Ala Asp Ala Gly Glu		
230	165	170	175
232	Gly Met Lys Trp Leu Tyr Lys Gln Ala Gln Ala Thr Gly Arg Ile His		
233	180	185	190
235	Phe Val Asn Gly Lys Val Thr Glu Leu Val Thr Glu Gly Asp Arg Val		
236	195	200	205
238	Ile Gly Ala Lys Leu Ser Asp Ser Lys Ile Leu Lys Ala Asp Val Val		
239	210	215	220
241	Met Val Ala Ala Gly Ala Trp Ser Gly Ser Leu Val Asp Leu Arg Gly		
242	225	230	235
244	Arg Thr Glu Ala Thr Gly His Ala Val Ala Tyr Met Asp Ile Thr Pro		
245	245	250	255
247	Glu Glu Gln Lys Arg Leu Asp Asn Phe Pro Val Val Leu Asn Leu Ser		
248	260	265	270
250	Thr Gly Leu Phe Leu Ile Pro Pro Arg Asn Asn Val Leu Lys Ala Ala		
251	275	280	285
253	Arg His Thr Phe Gly Tyr Ile Asn Pro Val Lys Ile Asn Asn Ala Leu		
254	290	295	300
256	Pro Pro Ser Pro Asn Asp Lys Arg Glu Pro Phe Ile Ala Ser Gln Pro		
257	305	310	315
259	Tyr Thr Ser Arg Asn Asp Ser Ser Asn Pro Leu Thr Val Glu Ala Asp		
260	325	330	335
262	Lys Asp Leu Arg Arg Ala Leu Thr Asp Leu Cys Pro Ile Arg Gly Leu		
263	340	345	350
265	Glu Thr Arg Pro Trp Lys Glu Ala Arg Ile Cys Trp Tyr Ser Asp Thr		
266	355	360	365
268	Arg Asp Gly Glu Trp Leu Ile Asp Tyr His Pro Gly Trp Lys Gly Leu		
269	370	375	380
271	Phe Val Ala Thr Gly Asp Ser Gly His Gly Phe Lys Phe Leu Pro Asn		
272	385	390	395
274	Leu Gly Glu Lys Ile Val Asp Val Met Gln Gly Gln Gly Lys Leu		
275	405	410	415

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277 Gly Glu Lys Trp Arg Trp Lys Glu Ile Gln Asn Asp Gly Val Gly Arg
 278 420 425 430
 280 Glu Thr Asn Gly Val Tyr Thr Gly Leu Val Thr Glu Asp Gly Ser Arg
 281 435 440 445
 283 Gly Gly Arg Pro Leu Val Leu Cys Asp Glu Leu Glu Lys Gly Arg Ala
 284 450 455 460
 286 Leu Ile Gly Asn Thr Lys Ala Lys Leu
 287 465 470
 290 <210> SEQ ID NO: 5
 291 <211> LENGTH: 1335
 292 <212> TYPE: DNA
 293 <213> ORGANISM: Fusarium proliferatum
 295 <220> FEATURE:
 296 <221> NAME/KEY: CDS
 297 <222> LOCATION: (1)..(1332)
 300 <400> SEQUENCE: 5
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 302 Met Ala Arg Thr Val Ala Pro Leu Asn Lys Asp Ser Gly Ile Leu Ile
 303 1 5 10 15
 305 gtt ggt ggc gga act tgg gga tgc tca act gcc ctc cat ctc gcc cgt 96
 306 Val Gly Gly Thr Trp Gly Cys Ser Thr Ala Leu His Leu Ala Arg
 307 20 25 30
 309 cgg ggt tac acc aac gtc act gtt ctc gat gtc aat cgc atc ccg tca 144
 310 Arg Gly Tyr Thr Asn Val Thr Val Leu Asp Val Asn Arg Ile Pro Ser
 311 35 40 45
 313 ccg ata tca gcc ggg cat gat gta aac aaa ctt tct aac aga cta ggc 192
 314 Pro Ile Ser Ala Gly His Asp Val Asn Lys Leu Ser Asn Arg Leu Gly
 315 50 55 60
 317 act tct gat agt aaa ggc gat gac gaa gac tca atc tgg aaa gct ctt 240
 318 Thr Ser Asp Ser Lys Gly Asp Asp Glu Asp Ser Ile Trp Lys Ala Leu
 319 65 70 75 80
 321 acg tac gcc gca gct caa gga tgg ctc cat gat ccc atc ttc caa cct 288
 322 Thr Tyr Ala Ala Ala Gln Gly Trp Leu His Asp Pro Ile Phe Gln Pro
 323 85 90 95
 325 ttc tgc cac aat aca gga gct gtc atg gct ggc tca aca cca aaa tct 336
 326 Phe Cys His Asn Thr Gly Ala Val Met Ala Gly Ser Thr Pro Lys Ser
 327 100 105 110
 329 atc aag cag ctg gta gaa gat gag atc ggt gac gac atc gac cag tat 384
 330 Ile Lys Gln Leu Val Glu Asp Glu Ile Gly Asp Asp Ile Asp Gln Tyr
 331 115 120 125
 333 aca cct ctc aac aca gca gaa gat ttc aga agg act atg ccg gag cgt 432
 334 Thr Pro Leu Asn Thr Ala Glu Asp Phe Arg Arg Thr Met Pro Glu Arg
 335 130 135 140
 337 att ctg aca ggt gat ttt cta ggc tgg aag ggc ttt tac aag ccc aga
 338 Ile Leu Thr Gly Asp Phe Leu Gly Trp Lys Gly Phe Tyr Lys Pro Arg
 339 145 150 155 160
 341 ggt tca ggt tgg gtt cat gcc aga aag gct atg aaa gct gct ttt gaa
 342 Gly Ser Gly Trp Val His Ala Arg Lys Ala Met Lys Ala Ala Phe Glu
 343 165 170 175

VERIFICATION SUMMARY

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